Conférence invitee

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Evolutionary dynamics of hom(oe)ologous chromosome segments within the highly polyploid sugarcane genome

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Modern sugarcane (*Saccharum* spp.) is the leading sugar crop and a primary energy crop. It presents one the most complex crop genome studied to date, mainly due to the very high level of vertical redundancy (2n = ca 12x = ca 120 = 10 Gb), together with an interspecific origin. Modern cultivars are derived from hybridization, performed by breeders a century ago, between two autopolyploid species, namely *S. officinarum* (domesticated, 2n=8x=80) and *S. spontaneum* (wild species, 2n=5x=40 to 16x=128).
To investigate genome dynamics in this highly polyploid context, we sequenced and analyzed the structural organization of hom(oe)ologous chromosome segments (bacterial artificial chromosome clones) from a few regions the sugarcane cultivar R570. For all regions, almost perfect gene colinearity and high gene structure and sequence conservation were observed. Moreover, the vast majority of the homoeologous genes were predicted, based on their structure, to be functional and showed signs of evolving under purifying selection. Compared to sorghum, the sugarcane haplotypes displayed a high gene colinearity. By contrast, transposable elements displayed a general absence of colinearity among hom(oe)ologous haplotypes
Our data suggest the presence of broad sets of functional homologous alleles in its genome, which could explain its unique efficiency, particularly its high phenotypic plasticity and wide adaptation.

Key words: Sugarcane, BAC sequence, hom(oe)ologous haplotypes, evolutionary dynamics